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OM nucleic - nucleic search, using sw model

Run on: July 11, 2003, 06:11:58 ; Search time 6704 Seconds  
(without alignments)  
17316.690 Million cell updates/sec

Title: US-10-053-662a-1

Perfect score: 3989  
Sequence: 1 tgggtcctccttattcacag.....ccagataatgctttattg 3989

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb\_ba: 2: gb\_hcg: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pat: 7: gb\_ph: 8: gb\_pl: 9: gb\_pr: 10: gb\_ro: 11: gb\_seg: 12: gb\_sy: 13: gb\_un: 14: gb\_vl: 15: em\_ba: 16: em\_fun: 17: em\_hum: 18: em\_in: 19: em\_mu: 20: em\_om: 21: em\_or: 22: em\_ov: 23: em\_pat: 24: em\_ph: 25: em\_pl: 26: em\_ro: 27: em\_seg: 28: em\_un: 29: em\_vl: 30: em\_hcg\_hum: 31: em\_hcg\_inv: 32: em\_hcg\_other: 33: em\_hcg\_mus: 34: em\_hcg\_pln: 35: em\_hcg\_rod: 36: em\_hcg\_mam: 37: em\_hcg\_vrt: 38: em\_sy: 39: em\_hugo\_hum: 40: em\_hugo\_mus: 41: em\_hugo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID        | Description         |
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| 1          | 2986.2 | 74.9        | 5200   | 6  | AX045561  | AX045561 Sequence   |
| 2          | 2986.2 | 74.9        | 5200   | 6  | 162749    | 162749 Sequence 12  |
| 3          | 2986.2 | 74.9        | 5200   | 9  | HSLAMB2T  | Z15008 H.sapiens m  |
| 4          | 2986.4 | 74.1        | 5156   | 6  | AX365737  | AX365737 Sequence   |
| 5          | 2956.4 | 74.1        | 5156   | 6  | HSNICE    | X73902 H.sapiens m  |
| 6          | 2944.2 | 73.8        | 3720   | 6  | AX045565  | AX045565 Sequence   |
| 7          | 2880.8 | 72.2        | 3620   | 6  | AX045567  | AX045567 Sequence   |
| 8          | 2879.2 | 72.2        | 5020   | 6  | AX045563  | AX045563 Sequence   |
| 9          | 2726   | 68.3        | 4316   | 6  | 162750    | 162750 Sequence 14  |
| 10         | 2726   | 68.3        | 4316   | 9  | HSLAMB2TB | Z15009 H.sapiens m  |
| 11         | 2652.2 | 66.5        | 5158   | 10 | MMU43327  | U43327 Mus musculus |
| 12         | 2590   | 64.9        | 5159   | 6  | AX045569  | AX045569 Sequence   |
| 13         | 2537.4 | 63.6        | 5057   | 6  | AX045571  | AX045571 Sequence   |
| 14         | 860.2  | 21.6        | 1393   | 10 | MUSNICC   | L20477 Mus musculus |
| 15         | 528.2  | 13.2        | 3020   | 5  | AF373841  | AF373841 Gallus ga  |
| 16         | 517.4  | 13.0        | 7642   | 10 | MUSLAMB2B | J03484 Mouse lamin  |
| 17         | 515.6  | 12.9        | 4948   | 6  | AX045115  | AX045115 Sequence   |
| 18         | 515.6  | 12.9        | 4948   | 6  | AX045332  | AX045332 Sequence   |
| 19         | 515.6  | 12.9        | 4948   | 6  | AX463752  | AX463752 Sequence   |
| 20         | 515.6  | 12.9        | 4972   | 6  | AX045119  | AX045119 Sequence   |
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| 23         | 515.6  | 12.9        | 5306   | 6  | AX463750  | AX463750 Sequence   |
| 24         | 515.6  | 12.9        | 5306   | 6  | HUMLAMB   | J03202 Human lamin  |
| 25         | 515.6  | 12.9        | 5330   | 6  | AX045117  | AX045117 Sequence   |
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| 28         | 514.6  | 12.9        | 7263   | 6  | AX045336  | AX045336 Sequence   |
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| 30         | 514.6  | 12.9        | 7554   | 6  | AX045121  | AX045121 Sequence   |
| 31         | 514.6  | 12.9        | 7554   | 6  | AX045334  | AX045334 Sequence   |
| 32         | 514.6  | 12.9        | 7554   | 6  | AX463754  | AX463754 Sequence   |
| 33         | 514.6  | 12.9        | 7554   | 10 | MUSLAMB2A | J02930 Mouse lamin  |
| 34         | 464.2  | 11.6        | 6055   | 5  | AF468048  | AF468048 Danio rer  |
| 35         | 366.8  | 9.2         | 551    | 6  | AX302928  | AX302928 Sequence   |
| 36         | 350.2  | 8.8         | 5184   | 9  | AF041835  | AF041835 Homo sapi  |
| 37         | 284.8  | 7.2         | 5737   | 3  | DROLAMB2  | M25063 Drosophila   |
| 38         | 284.8  | 7.1         | 4482   | 3  | DROLAMB2  | X07806 Drosophila   |
| 39         | 265.2  | 6.6         | 1778   | 6  | AX333505  | AX333505 Sequence   |
| 40         | 265.2  | 6.6         | 1778   | 9  | HSLAMB124 | U31201 Human lamin  |
| 41         | 265.2  | 6.6         | 164084 | 9  | AL354953  | AL354953 Human DNA  |
| 42         | 265.2  | 6.6         | 170492 | 2  | AL139013  | AL139013 Homo sapi  |
| 43         | 263.6  | 6.6         | 220000 | 2  | AC004795  | AC004795 Homo sapi  |
| 44         | 239    | 6.0         | 5153   | 10 | AF083372  | AF083372 Mus muscu  |
| 45         | 234.8  | 5.9         | 4664   | 10 | AF079520  | AF079520 Mus muscu  |

ALIGNMENTS

RESULT 1  
AX045561  
LOCUS AX045561 5200 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 25 from Patent WO0066731.  
ACCESSION AX045561  
VERSION AX045561.1 GI:11344011  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 5200)  
AUTHORS Boutaud,A.  
TITLE Recombinant laminin 5  
JOURNAL Patent: WO 0066731-A 25 09-NOV-2000;

BioStatum, Inc. (US)  
 Location/Qualifiers  
 1.5200  
 /organism="Homo sapiens"  
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 519 peptide  
 BASE COUNT 1364 a 1236 c 1392 g 1208 t  
 Query Match 74.9%; Score 2986.2; DB 6; Length 5200;  
 Best Local Similarity 88.5%; Pred. No. 0;  
 Matches 3328; Conservative 0; Mismatches 403; Indels 30; Gaps 7;

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 Qy 1652 CCCCCAGGGTGTCACTGCTGCTGCTGAGCTGTGTGCTGATGTGCTATTTTGGGAGCC 1711  
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|            |  |            |     |        |                 |
|------------|--|------------|-----|--------|-----------------|
| RESULT 2   |  |            |     |        |                 |
| LOCUS      | 162749                                   | 5200 bp    | DNA | linear | PAT 07-OCT-1997 |
| DEFINITION | Sequence 12 from patent US 5660982.      |            |     |        |                 |
| ACCESSION  | 162749                                   |            |     |        |                 |
| VERSION    | 162749.1                                 | GI:2480457 |     |        |                 |
| KEYWORDS   | .  |            |     |        |                 |
| SOURCE     | Unknown.                                 |            |     |        |                 |
| ORGANISM   | Unknown.                                 |            |     |        |                 |
| REFERENCE  | Unclassified.                            |            |     |        |                 |
| AUTHORS    | 1 (bases 1 to 5200)                      |            |     |        |                 |
| TITLE      | Trygvason, K., Kallunki, P. and Pyke, C. |            |     |        |                 |
| JOURNAL    | Laminin chains: diagnostic uses          |            |     |        |                 |
| FEATURES   | Patent: US 5660982-A 12 26-AUG-1997;     |            |     |        |                 |
|            | Location/Qualifiers                      |            |     |        |                 |
|            | 1..5200                                  |            |     |        |                 |
|            | /organism="Unknown"                      |            |     |        |                 |
| BASE COUNT | 1364 a 1236 c 1392 g 1208 t              |            |     |        |                 |
| ORIGIN     |  |            |     |        |                 |

| Query Match | Similarity | Score  | DB  | Length                            |
|-------------|------------|--|-----|-----------------------------------|
| Local       | 88.5%      | 2986.2   | 6   | 5200                              |
| Matches     | 3128       | Conservative   | 0   | Mismatches 403; Indels 30; Gaps 7 |
| QY          | 99         | AAGGAAAAGGAAGGACACAGCGGAGCGCAGATGTAGAACTCCAGCGCGGAGCGCCCGGC    | 158 |                                   |
| Db          | 14         | AAGGAAAAGGAAGGACACAGCGGAGCGCAGATGTAGAACCAACCAAC--CGAGCGCCGGGC  | 71  |                                   |
| QY          | 159        | AGCGACCCCTGCAAGCGGCGG-----GACCGCGCGCGCGGCGTGGCCATGCTCGGCTCTG   | 211 |                                   |
| Db          | 72         | AGCGACCCCTGCAAGCGGAGGACAGAGCTGAGGGGGCGCGGCAACCGCATGCTGGGCTCTG  | 131 |                                   |
| QY          | 212        | GCTGAGCTGCTAAGCTCTGCTCTCTGCTCTCTCTGCGAGCGCGGCGCACTCCGGAG       | 271 |                                   |
| Db          | 132        | GCTGGGCTGCTGCTG    | 191 |                                   |
| QY          | 272        | GGAAGCTCTGTGATTTGCCAACGGGAAGTCCAGGCAATGCACTTTTGAACAGAACTTCAACA | 331 |                                   |
| Db          | 192        | GGAAGCTCTGTGATTTGCCAATGGGAAGTCCAGGCAAGTATCTTTGATCGGGAATCTTCAAG | 251 |                                   |
| QY          | 332        | ACAGACAGGAATGGAATTCGGCTGCTCACTGCAATGCAACAACTGATGGCATTCACATG    | 391 |                                   |
| Db          | 252        | ACAAATCTGTATGGATTCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG | 311 |                                   |
| QY          | 392        | CGAGAGGTGCAAGCGAGGATTTTACCGACAGAGAGAAAGGAGCCGCTGTTTACCTGCA     | 451 |                                   |
| Db          | 312        | CGAGAGGTGCAAGGATGGCTTTTACCGGCAAGAGAAAGGAGCCGCTGTTTGGCCTGCA     | 371 |                                   |
| QY          | 452        | TTGTACTCTTAAAGGTTCTCTTACGCGTGCATGTGACAACTCTGACGGTGCAGCTGTA     | 511 |                                   |
| Db          | 372        | TTGTACTCTTAAAGGTTCTCTTACGCGTGCATGTGACAACTCTGACGGTGCAGCTGTA     | 431 |                                   |
| QY          | 512        | GCCAGGTGTACAGAGACAGGTGTGACCGATGTGCTGCCCGGCTTCCACACATTCATGTA    | 571 |                                   |
| Db          | 432        | ACCAGGTGTGACAGAGACCAATGTGACCGATGTGCTGCCAGGCTTCCACATGCTCACGGA   | 491 |                                   |
| QY          | 572        | TGCTGGGCGGCGCCCAAGACCAAGGCTGCTGACCTCAAGTGTGACTGTGACCCAGCGTG    | 631 |                                   |
| Db          | 492        | TGCGGGGTCACCCCAAGACCAAGGCTGCTGACCTCAAGTGTGACTGTGACCCAGCGTG     | 551 |                                   |
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| Db          | 552        | CATGCGAGGCGCTGTGACTCAGGCGCGGCGCTGTGTGCAAGCGCGGCTGTCACTTGAGAGCG | 611 |                                   |
| QY          | 692        | CTGTGATGAGTGTGACACCGATTACTACCTGTGATGGGGAAACCTTCAGGGCTGTAC      | 751 |                                   |
| Db          | 612        | CTGTGATGAGTGTGATCAGGTTACTATAACTGTGATGGGGGAAACCTTCAGGGCTGTAC    | 671 |                                   |
| QY          | 752        | CCAAGTCTTTTGTGATGGGCAATTCGCGCAGCTGCCACAGCTCTGGGGACTTACAGTGTCA  | 811 |                                   |
| Db          | 672        | CCAAGTCTTTTGTGATGGGCAATTCAGCAGCTGCCAGCTCTGGAGAAATACAGTGTCA     | 731 |                                   |
| QY          | 812        | TAAATATCTCTGCTTCCATCAAGATGTTGATGGCTGGAAGGCTGTCCAAAGAACG        | 871 |                                   |

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| Db | 732  | TAAGATACCTCTACCTTTTATCAAGATGTTGATGGCTGGAAAGCTGTCCAAACGAATGG        | 791  |
| Oy | 872  | GTCCTCGCAAGCTCCAGTGTGCACAGCCCATCGGGATATATTAGCTACGACGACG            | 931  |
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| Oy | 932  | ATCAGACCCTGTATTTTGTAGAGTCCGTGGCAAAATTTCTTGGGAATCAACAGGAGACTA       | 991  |
| Db | 852  | ACTAGATCTGTCTATTTTGTGGGTCTGTGCAAAATTTCTTGGGAATCAACAGGAGACTA        | 911  |
| Oy | 992  | CGGCAAAAGCTATCTTTGACTACCCGTGTGATAGGGAGGACGACACCATCTGCGCA           | 1051 |
| Db | 912  | TGGGCAAAAGCTGTCTTTGACTACCCGTGTGAGACAGAGAGGACGACACCATCTGCGCA        | 971  |
| Oy | 1052 | TGACGTATCTGGAAAGTGTGTGTCTACGAGATCACAGCTCCCTTGATGCCACTTACAA         | 1111 |
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| Oy | 1112 | GACACTCCCTTGGGGATCAACAAAGATTTCACATTCAGATTAAATGAATCATCAACAG         | 1171 |
| Db | 1032 | GACACTCCCTTGGGGCTCACCAAGATTTCACATTCAGATTAAATGAGATCCAAACAA          | 1091 |
| Oy | 1172 | TAATTGAGCCCCCAGCTAAGTTACTTTGAGTATCGAGGTTACTGCGGAACCTCACAGC         | 1231 |
| Db | 1092 | TAATTGAGCCCCCAGCTGAGTTACTTTGAGTATCGAAGTTACTGCGGAATCTCACAGC         | 1151 |
| Oy | 1232 | CTGCGGATCCGAGCTACCTACGGAAGATACAGTACTGGGTAATTGACAACTGACCTT          | 1291 |
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| Db | 1749 | CACAGCCGGGATCTACTGTGCACACAGTGTCAAAAGCAGCTACTTCCGGGGACCCCATTTGGCTCC | 1808 |
| Oy | 1892 | CAATTCAGCAAGATGTGAGCTTGCACTGCAATCCAGTGGGCTCCGAGCTGTGGA             | 1951 |

Db 1809 CAACCCAGCAGACAGTGTGAGCTTGCAACTGTAACTCCCATGGGCTCAGAGCCCTGTAGG 1868  
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 Kallunki,P., Sainio,K., Eddy,R., Byers,M., Kallunki,T., Sariola,H.,  
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 A truncated laminin chain homologous to the B2 chain: structure,  
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Journal  
J. Cell Biol. 119 (3), 679-693 (1992)  
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2 (bases 1 to 5200)  
AUTHORS  
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Direct Submission  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1  
AUTHORS Wang, T., Wang, A., Skelky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,  
McNeill, E.D., Fanger, N., Retter, M.W., Marmaralis, M., Fanger, G.R.,  
Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.  
TITLE Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL Patent: WO 0200174-A 130 03-JAN-2002;  
CORIXA CORPORATION (US)  
FEATURES  
Source 1. 5156  
Location/Qualifiers  
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BASE COUNT 1351 a 1222 c 1377 g 1206 t  
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Query Match 74.1%; Score 2956.4; DB 6; Length 5156;  
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| DEFINITION  | Sequence 29 from Patent WO0066731.  |         |        |        |                 |
| ACCESSION   | AX045565  |         |        |        |                 |
| VERSION     | AX045565.1  |         |        |        |                 |
| KEYWORDS    | GI:11344015   |         |        |        |                 |
| SOURCE      | human.  |         |        |        |                 |
| ORGANISM    | Homo sapiens  |         |        |        |                 |
| REFERENCE   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.   |         |        |        |                 |
| AUTHORS     | 1 (bases 1 to 3720)   |         |        |        |                 |
| TITLE       | Boutlaud, A.  |         |        |        |                 |
| JOURNAL     | Recombinant laminin 5   |         |        |        |                 |
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|             | Biostatium, Inc. (US)   |         |        |        |                 |
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AUTHORS Boutaud A.  
TITLE Recombinant laminin 5  
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| QY | 3497 | TGGCATCCTACACCTAATAG | 3516 |
|    |      |                      |      |
| Db | 3426 | CGGCCTCTGCATCTGATGG  | 3445 |

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|------------|-----------------------------|---------|------|--------|-----------------|
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| LOCUS      |                             |         |      |        |                 |
| DEFINITION | H.sapiens mRNA for laminin. | 4316 bp | mRNA | linear |                 |
| ACCESSION  | Z15009.S47253               |         |      |        |                 |
| VERSION    | Z15009.1 GI:34231           |         |      |        |                 |
| KEYWORDS   | laminin.                    |         |      |        |                 |
| SOURCE     | Homo sapiens.               |         |      |        |                 |
| ORGANISM   | Homo sapiens                |         |      |        |                 |

| REFERENCE   | AUTHORS   | TITLE   | JOURNAL                               |
|---|---|---|---------------------------------------|
| 1 (bases 1 to 4316)   | Tryggvason, K.  | Direct Submission   | Submitted (27-AUG-1992)               |
| 2 (bases 1 to 4316)   | Oulu, Biochemistry, Linnamäe, Oulu, Finland, SF-90570 |   |                                       |
| Kallunki, P., Sainio, K., Eddy, R., Byers, M., Kallunki, T., Sariola, H., Beck, K., Hirvonen, H., Shows, T. B. and Tryggvason, K. |   | A truncated laminin chain homologous to the B2 chain: structure, spatial expression, and chromosomal assignment | J. Cell Biol. 119 (3), 679-693 (1992) |
| 93016279  |   |   |                                       |
| PUBMED  |   |   | 1383240                               |

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ORIGIN

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| Best Local Similarity | 88.5%        | Pred. NO. 0 |                |             |
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|                       |              |             |                | Gaps 7      |

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| Db | 14   | AAGGAAAAGGAGCAGCGAGGACCGAGATGGAATCCAGCGGCGAGGCGCCGGG             | 71   |
| OY | 159  | AGCGACCCCTTGACAGGGCG-----GACCGCGCGCGGCGCTTGCCATGCTGCGCTCTG       | 211  |
| Db | 72   | AGCGACCCCTTGACAGCGGAGCAGAGACTGAGCGGCGCGGACCGGCGCATGCTGCGCTCTG    | 131  |
| OY | 212  | GCTAGGCTGCTACCTCTGCTCTTCCGCTCCACTGCGCCGAGCCCGGGCCACCTCCGGAG      | 271  |
| Db | 132  | GCTGGGCTGCTGCTCTGCTCTTCCGCTCTCTGCTCCGAGCCCGGGCCACTCTCCAGAG       | 191  |
| OY | 272  | GGAAGTGTGATTTGCCAAGGGAAGTCCAGGCAATGCATCTTTGACAGGAATTCAAA         | 331  |
| Db | 192  | GGAAGTGTGATTTGCCAATGGAAGTCCAGGAGTGTATCTTTGATCGGGAATTTCAAG        | 251  |
| OY | 332  | ACAGACAGGAATGGAATTTCCGCTGCCCTCACTGCAATGACAAACATGAGCATCCACTG      | 391  |
| Db | 252  | ACAAACGTGGAATGGAATTTCCGCTGCCCTCACTGCAATGACAAACATGAGCATTCCTG      | 311  |
| OY | 392  | CGAAGGTGACAGGACAGGATTTTACCACAGAGAAAGGACCGCTGTTTACCCTGCAA         | 451  |
| Db | 312  | CGAAGTGTGCAAGATGGCTTTTACCGGGCAAGAGAAAGGACCGGCTGTTTACCCTGCAA      | 371  |
| OY | 452  | TTGTAACTCTAAGGTTCTCTTAGCGCTCGATGTGACAACTCTGACGGTGGAGCTGTAA       | 511  |
| Db | 372  | TTGTAACTCTCAAGGTTCTCTTAGTGTCTCAATGTGACAACTCTGAGGGTGGAGCTGTAA     | 431  |
| OY | 512  | GCCAGGTGTGACAGAGACAGGTGTGACCGATGTCTGCGGGCTTCCACACATCCATGA        | 571  |
| Db | 432  | ACCAGGTGTGACAGAGACAGATGTGACCGATGTCTGCGAGGCTTCCACATGCTCAAGGA      | 491  |
| OY | 572  | TGCTGGGTGCGCCCAAGACCAAGGCTGTAGACTCCAAAGTGTGACTGTGACCCAGCTGG      | 631  |
| Db | 492  | TGCGGGGTGACCCCAAGACCAAGACTGTAGACTCCAAAGTGTGACTGTGACCCAGCTGG      | 551  |
| OY | 632  | CATCTCAGGGCCCTGTGATCAGGGCCGCTGTGTGTGAAGCGCGGCTGTCACTGAGAGCG      | 691  |
| Db | 552  | CATGCGAGGGCCCTGTGATCAGGGCCGCTGTGTGTGAAGCGCACTGTATTGAGAGAGCG      | 611  |
| OY | 692  | CTGTGATAGGTGTGACACAGGTTACTATCACTTGATGAGGGAAACCTCAGGGCTGTAC       | 751  |
| Db | 612  | CTGTGATAGGTGTGTGATCAAGGTTACTATCACTTGATGAGGGGAAACCTCAGGGCTGTAC    | 671  |
| OY | 752  | CCAGTGTCTTGTCTATGSGGCAATTCGCGCAGCTGCCACAGCTCTGSGGACATCAAGTGTCCA  | 811  |
| Db | 672  | CCAGTGTCTTGTCTATGSGGCAATTCAGCGCAGCTGCCACAGCTCTGSGGAATCAAGTGTCCA  | 731  |
| OY | 812  | TAAATATATCTCTGACCTTCCATCAAGATGTTGATGGCTGGAAGGCTGTCCAAATAAACG     | 871  |
| Db | 732  | TAAATATATCTCTACCTTTCACTCAAGATGTTGATGGCTGGAAGGCTGTCCAAATAATG      | 791  |
| OY | 872  | GTCCTCTGCAAAAGCTCAGATGTGACAGCGCCATCGGGATATATTAGCTCAGACGAGCG      | 931  |
| Db | 792  | GTCCTCTGCAAAAGCTCCAAATGTGACAGCGCCATCAAGATGTGTTAGCTCAGCGCCAGCG    | 851  |
| OY | 932  | ATCAGACCCCTGTCTATTTTGTAGTCTCCAGCAATTTCTTGSGGAATCAACAGGTGAGCTA    | 991  |
| Db | 852  | ACTAGATCTGTGTCTATTTTGTGSGCTCTGCGCAAAATTTCTTGSGGAATCAACAGGTGAGCTA | 911  |
| OY | 992  | CGGCAAAAGCTATCTTTTGTGACTACCGGTGTGATAGGGGAGGACAGACCCCATGTGCCA     | 1051 |
| Db | 912  | TGGGCAAAAGCTGTCTTTTGTACTACCGGTGTGACAGAGAGGACAGACCCCATGTGCCA      | 971  |
| OY | 1052 | TGACGTGATCTGGAAGGTGTGATGTCTACCGATACAGCTTCCCTTGATGCCACTTAAAGAA    | 1111 |
| Db | 972  | TGATGTGATCTTGGAAGGTGTGATGTCTACCGATACAGCTTCCCTTGATGCCACTTAAAGAA   | 1031 |
| OY | 1112 | GACACTGCTTGTGGGAATCAACAAGACTTACACATTCAGATTAAATGAAATCCAAAGAG      | 1171 |
| Db | 1032 | GACACTGCTTGTGGGCTACCAAGACTTACACATTCAGATTAAATGAGATCCAAAGAA        | 1091 |

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|----|------|---|------|
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| Db | 1092 | TAATTGGAGCCCCCGACTAGTACTTTGAGTATCGAAGGTTACTCGGAACTTCACAGC             | 1151 |
| QY | 1232 | CCTGGGAAATCGAGGTACTCGTACCGGAATPACAGTCTGGGTACATGTGCAACGTGACCTT         | 1291 |
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| QY | 1292 | GATTTCAAGCCGCCCCGTTTCTGAGAGCCCCAGCGCCCTGGGTTGAAACATGTGATGCC           | 1351 |
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| QY | 1352 | TGTTGGCTACAAAGGGGCAATTCTGCGAGATTTGTCTTCTGGCTACAAAGAGATTGAGC           | 1411 |
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| Db | 1332 | GAGACTGGGACCTTTTGGCACCCTGTATTTCTGTGACCTGTCAAGGGGAGGGGCTGTGGA          | 1391 |
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| QY | 1592 | TTCGAATGGGTCAAGCTGCTCCGTGATGCCCTGAGACACAGAGAGTGTGTGCATTAATCTG         | 1651 |
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| QY | 1652 | CCCCCAGGGGTGACATGTGTGCCCGGTGTGAGCTCTGTCTGATGAGCTATTTTGGGGAGCC         | 1711 |
| Db | 1569 | CCCTCCCGGGGTGACCGGTTGCCGCTGTGAGACTCTGTCTGATGAGCTATTTTGGGGAGCC         | 1628 |
| QY | 1712 | CTTGGGGAAAGCTGGCCCAAGTAGAGGCTTGTACGCCCTGTGACGTGCAACAAAGCTGGA          | 1771 |
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| QY | 1772 | CCCTAATGCCCTCCGGGAACTGTGACCCGCTGACAGGCAAGGTGTCTGAAGTGCATTCACAA        | 1831 |
| Db | 1689 | CCCCAGTCCCTCTGGGAAATTGTGACCCGGCTGACAGGCAAGGTGTGAAGTGTATTCACAA         | 1748 |
| QY | 1832 | CACAGCTGGGGTCCACTGTGTGACACAGTGTGAAGAAAGCAGGCTACATATGGGGGACCGGTTGGCTCC | 1891 |
| Db | 1749 | CACAGCCGGGACTCTACTGCGACAGTGTGAAGAAAGCAGGCTACTTTGGGGACCCATTGGCTCC      | 1808 |
| QY | 1892 | CAATCAGCAGACAAAGTGTGCAAGCTTGCACACTGCAACCCAGTGGGCTTCGAGCCTGTGGA        | 1951 |
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| QY | 1952 | GTGTGAAAGTATGGCAGCTGTGTGTTGCAAGCCAGGCTTTGGTGCTCAGCTGTGACA             | 2011 |
| Db | 1869 | ATGTGGAAGTATGGCACTGTGTGTTGCAAGCAGAGATTTGGTGCCCCCAACTGTGTGACA          | 1928 |
| QY | 2012 | TGCGGCACTGACACAGCTGTCCAGCTTGTCTATTAATCAATGTGAAGTTCAAGATGCAT           | 2071 |
| Db | 1929 | TGAGACATT---CAGCTGTCCAGCTTGTCTATTAATGAATGAAAGATTCAAGATGCAT            | 1985 |
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| Db | 1986 | TATGCAAGAGCTTCAGAAATGGAAGCCCTGATTTCAAAAGCTCAGGCTGTGATGTGAGT           | 2045 |
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|----|------|--|------|
| Db | 2166 | GGTGGAGGCCAAGAAAGAGCTTCCAGAGCCGCTTGAGATGACCTCAAGATGACTGTGGA    | 2225 |
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| Qy | 2366 | CAGTCAGATGCGCTGAGCCTGAGAGAAAGTGAAGGCTTCCCTGCAAAACCAACATATCC    | 2425 |
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| Qy | 2426 | TCCTTCAGAGCACTACGTTGGGCAAAATGCTTTAAAGTCTGTGCTCAGAGAGCCACAG     | 2485 |
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QY 3377 GGAGCAGAGTTTGAACATGATATGACGAGAGCCAGATGATTAATGCACAGCCCAAG 3436

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QY 3437 AGTTGAAAAGAGCCAGAAATGCTGAGTTTACATCAAGACACTCAACATTGA 3496

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 5158)  
AUTHORS Yamada, Y.  
TITLE Direct Submission  
JOURNAL Submitted (13-DEC-1995) Laboratory of Developmental Biology,  
National Institute of Dental Research, National Institutes of  
Health, 9000 Rockville Pike, Bethesda, MD 20892, USA  
2 (bases 1 to 5158)  
AUTHORS Sugiyama, S., Uchida, A., Yamada, S., Kozak, C.A. and Yamada, Y.  
TITLE Cloning and expression of the mouse laminin gamma 2 (B2t) chain, a  
subunit of epithelial cell laminin  
JOURNAL Eur. J. Biochem. 228 (1), 120-128 (1995)  
PUBMED 9518894  
7882992

REFERENCE 3 (bases 1 to 5158)  
AUTHORS Sasaki, T., Gohring, W., Mann, K., Brakebusch, C., Yamada, Y.,  
Fassler, R. and Timpl, R.  
TITLE Short arm region of laminin-5 gamma2 chain: structure, mechanism of  
processing and binding to heparin and proteins  
JOURNAL J. Mol. Biol. 314 (4), 751-763 (2001)  
PUBMED 21592560

REFERENCE 4 (bases 1 to 5158)  
AUTHORS Sasaki, T. and Yamada, Y.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-2002) Laboratory of Developmental Biology,  
National Institute of Dental Research, National Institutes of  
Health, 9000 Rockville Pike, Bethesda, MD 20892, USA  
REMARK COMMENT  
FEATURES  
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 AUTHORS Boucaud, A.  
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 DB 3622 TGTCTATGAGATTTGTCTCAC 3641

RESULT 13  
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 LOCUS AX045571 5057 bp DNA linear PAT 24-NOV-2000  
 DEFINITION Sequence 35 from Patent WO0066731.  
 ACCESSION AX045571.1 GI:11344021  
 VERSION AX045571.1  
 KEYWORDS house mouse.

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 5057)  
 AUTHORS Bouteaud, A.  
 TITLE Recombinant laminin 5  
 JOURNAL Patent: WO 0066731-A 35 09-NOV-2000;  
 Biostatium, Inc. (US)  
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 Best Local Similarity 83.0%; Pred. No. 0;  
 Matches 2944; Conservative 1; Mismatches 582; Indels 18; Gaps 4;  
 QY 261 ACCTCGGAGGGAATCTGTATGCAACGGGAATCCAGGAATGCATCTTTGACCG 320  
 DB 1 ACCTCAGAGGGAATCTGTATGCAATGGGAATCCAGGAATGTGCTTTGATCAG 60  
 QY 321 GAACCTCACAAACAGACAGAAATGATTCCGCTGCTCAACTGCATGACAACTGAT 380  
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 QY 381 GGCATCACTGCGAGAGGTGCAAGGAGATTTTACCGACAGAGAAAGGACCGCTGT 440  
 DB 121 GGGGTTCACTGCGAGAGGTGCAAGGAGGAGGTTTACACACATCAGAGCAAGCCGCTGC 180  
 QY 441 TTACCTGCAATTGTAATCTTAAAGTTCTTTAGGCTCGATGTGACAACTTGAACGG 500  
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 DB 241 TGCAGGTGAAGCAGGTGTGACAGAGCAAAAGATGTGACAGTGTGACCGAGCTTCCAT 300  
 QY 561 ACACTCACTGATGCTGGATGCGGCCAAGCAAAAGGCTCTAGACTCCAAGTGTGACTGT 620  
 DB 301 ATGCTCACCGATGCTGATGACACCGAGACAGGCGCACTAGATTCCAAGTGTGACTGT 360  
 QY 621 GACCCAGCTGGCATCTCAGGCGCTGTGACTCAGGCGCTGTGTCTGCAAGCGCGCTGT 680  
 DB 361 GACCCAGCTGGCATCTCAGGCGCTGTGACTCAGGCGCTGTGTCTGCAAGCGCGCTGT 420

|    |      |   |      |
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| QY | 661  | ACTGAGAGCGCTGTGATAGGTGTGACACAGATTACTATGACTGTGAGTGGGGAAACCT      | 740  |
| Db | 421  | ACTGAGAGCGCTGTGATAGGTGTGCGACACAGTGACTATCATCTGGACCCGGCAACCTT     | 480  |
| QY | 741  | CAGGCGCTGTACCCAGTGTGTTTGTCTATGGGCAATTCGGCACCTGCACAGCTCTGGGAC    | 800  |
| Db | 481  | GAGGCGCTGTACCCAGTGTGTTTGTCTATGGGCAATTCAGCCAGCTGCCAGCTTCTGGCAC   | 540  |
| QY | 801  | TACAGTGTCCATAAATATCATCTGTGCTTCGCATCAAGATGTGATGGCTGGAGGCTGTC     | 860  |
| Db | 541  | TTCACTGTGCCAATAATACATTTCAACTTTGACTGAGATGTGATGGTGGAGGCGGTT       | 600  |
| QY | 861  | CAAGAAACCGGCTCTCTCTCCAAAGTCCAGTGTGTACAGCGCCCATCGGGATATATTAGC    | 920  |
| Db | 601  | CAGAGAAACGGGGCACCTCGCAAAATCTCACCTGTGTACAGCCCATTCGGAGTGTAGT      | 660  |
| QY | 921  | TCAGCAGACGATTCGACCCCTGTCTATTTTGTAGTCCCTGTCCAAATTTCTTGGGAATCA    | 980  |
| Db | 661  | TCGTCCCGAAGATCAGACCCCGTCTATTTTGTGGCCCTGTGCCAAATTCCTCGTAAACAG    | 720  |
| QY | 981  | CAGGTGACCTACGGGCAAAAGCTATCTTTTGACTACCGTGTGATAGGGAGGAGACAC       | 1040 |
| Db | 721  | CAAGTGAATTAAGGGCAAGCGCTGTCTTTTACTACACGCGGTGTGACAGAGAGTAAACAG    | 780  |
| QY | 1041 | CCATGTGCCCATGACGTATCTCTGGAAGTGTGTGTCTTACGAGATCACGTCCTTGATG      | 1100 |
| Db | 781  | CCGTGTGCTCTAGATGTATCTCTGGAAAGTGTGTGTCTTCAAGATCAGAGCTCTCTGATG    | 840  |
| QY | 1101 | CCACTTACCAAGACATGCGCTTTGTGGGATTCACAAAGATTACACTTCAGATTAAATGAA    | 1160 |
| Db | 841  | GCTCAGGAAAGACATTCCTTGTGGGATTCACAAAGATTACACTTCAGACTAAATGAA       | 900  |
| QY | 1161 | CATCCAAACAGTAATTTGAGGCCCCAGCTAGTTACTTTGAGTATCCGAGGTTTACTCGCG    | 1220 |
| Db | 901  | CATCCAAACAGTCACTGGAAGTCCCAAGTGAATTATTCGAATATCAGAGTTACTCGCG      | 960  |
| QY | 1221 | AACTCTACAGC---CTTCCGATTCGAGCTACTACGGAATAACAGTACTGGGTACATT       | 1277 |
| Db | 961  | AACTCTACAGCCTCTGTATATCCGAGCTACGTAACGGAATAATAGTACAGGTTACATT      | 1020 |
| QY | 1278 | GACAAACGACCTTGATTTTCAAGCCCGCCCGCTTCTGGAAGCCACAGCGCCCTGGGTTGAA   | 1337 |
| Db | 1021 | GATTAACGTAGCCCTGTGTTTCAAGCCCGCCCGCTTCTTGAAGCCACAGCCCTTGGGTTGAA  | 1080 |
| QY | 1338 | CAATGTGATGCCCTGTGGTGCCTACAAAGGGGAGTTCTGCACAGAAATGTGCTTCGGCTAC   | 1397 |
| Db | 1081 | CGTTGTGATGCTCTGCTGGGTACAAAGGAACAATTTCTCCACAGAAATGTGCTTGTGTTAC   | 1140 |
| QY | 1398 | AAAAAGATTCAGCCAGACGTGGGACCTTTTGGACCTGTATTTCACTGTAATGCCCAAGG     | 1457 |
| Db | 1141 | AAAAAGATTCGGCAAGATTTGGGCGCTTTTGGCGCGCTGTGTTCCCTGTAACTGCCAAGG    | 1200 |
| QY | 1458 | GAGGGGCGCTGCGATTCAGACACAGAGAACGTGTTACTAGGGGATGAGAACCTTGACATC    | 1517 |
| Db | 1201 | GAGGGGCGCTGTGATTCAGACACAGGGAATTTGCTACTGGGGGAGCAGAAATCTGTACAT-   | 1259 |
| QY | 1518 | CCTGAGTGTGCTGATGCGCCCATTTGGTTTCTTACAAGATTCACAAGAACCCCGACAGCTGC  | 1577 |
| Db | 1260 | --TGAGTGTGCTGATGTGTCCTATCGGTTTCTTACAATGACCCACATGACCCCGACAGCTGC  | 1317 |
| QY | 1578 | AAGCGGTGCCCTGTGCGAATGGGTTTCACTGCTCCGTATGCTCTGAGTCCGTGACAGAGAGTG | 1637 |
| Db | 1318 | AAGCATGTCCCTGTCAACAATGGGTTCAAGCTGTTCAGTGAAGTCCGTGACACAGAGAGTG   | 1377 |
| QY | 1638 | GTTGTCAATTACTGCCCCCAGGGGTCTACTGTGTCCGCTGTAGCTTGTGTGTGATGGC      | 1697 |
| Db | 1378 | GTTGTCAACTGTGCCCCCTGGGGGTCAAGGTGTCCGCTGTGAGCTCTGTGTGTGATGGC     | 1437 |
| QY | 1698 | TATTTTGGGAGCCCCCTTGGGGGAAAGTGGCCAGTGAAGGCTGTGACCCCTGTCAAGTG     | 1757 |
| Db | 1438 | TTCTTTGGGAGCTCTTTGGGGAACATGGCCAGTGAAGGCTTGTTCACAGCTGCCAATGC     | 1497 |
| QY | 1758 | AACAACAACGTGAGCCTTAGTGCCTTCGGGAACTGTGAACGCGCTGTACAGGACAGTGTCTG  | 1817 |

[illegible]



Db 303 CATCTCGAACCTTGATTTCTGAGGAGATGTCTGCAAAACAGCCGCTCATGAGAGCG 362  
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 QY 812 TAAATATCATCTGACCTTCATCAAGATGTGATGAGTGAAGGCTGTCCAAAGAAACGG 871  
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RESULT 15  
 AF373841 3020 bp mRNA linear VRT 22-MAY-2001

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 ACCESSION AF373841  
 VERSION AF373841.1 GI:14165135

KEYWORDS Gallus gallus.  
 SOURCE Gallus gallus.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 3020)  
 AUTHORS Halter, W., Dong, S., Balasubramani, M., and Bier, M.E.  
 TITLE Aberrant histogenesis after temporary disruption of the retinal  
 basal lamina  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3020)  
 AUTHORS Dong, S., Balasubramani, M., Halter, W., and Bier, M.E.  
 TITLE Direct Subnission  
 JOURNAL Submitted (26-APR-2001) Neurobiology, University of Pittsburgh,  
 3500 Terrace Street, Pittsburgh, PA 15261, USA  
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BASE COUNT 693 a 855 c 912 g 560 t  
 ORIGIN

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 QY 399 TGCAGGAGATTTTACCGACAGAGAAAGGACCGCTGTATTACCTGCAATTGTAC 458  
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 QY 639 GGGCCCTGTACTCAGCGCGCTGTGCTGCAAGCCGCGCTGTCACTGAGAGCGCTGTGT 698



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QY GSACTTTTGGCAGCTGTATTTCAATGTAATGCAATGCAAGG---GGAGGGGCTGGATCCA 1475
Db 1411 GGGCCCTTACAGCCCTGCTGCTTGTGCACTGTCAATGGGCAACGAGACCTGTGATCTT 1470
QY GACACAGAGACTGTACTAGGGGATAGAAACCTGACATCCCTGAGTGTGCTGACTGC 1535
Db 1471 GAGACGGGCGGTGCGACTGTAGGGAT---AACACGGCAGGCTCTCACTCGAAGATGC 1527
QY CCCATTGGTTTCTAACAGATCAACAAAGAC-----CCCGCAGCTGCAAGCCGTGCC 1589
Db 1528 AGCGATGGGTACTACGGGGATGCGACAGCGGGCACAGCTTGGACTCCAGCCCTGCCCC 1587
QY TGTGCGAAATGGTTCACTGCTCTCCGTGATGCTGTAGACAGAGAGGTGTGTGAATAAC 1649
Db 1588 TGCCCGCGGCGCTCAAGCTGTGCGTGTGCGCCGCAAAAGAGGTGTGTGACCCAGC 1647
QY TGCCCGCAGGATGCTCACTGTGCGCGCTGTGAGCTGTGCTGATGAGCTATTTTGGAGAC 1709
Db 1648 TGCCAGACAGGACCAACCGGAAGAGGTGTGAGCTGTGTGATGACGCTATTTTGGAGAC 1707
QY CCCTTTCGGGGAACGTGGCCCAAGTGAGGCTTTGTTCAGCTGTCAAGTCAACCAACGTG 1769
Db 1708 CCACTGGGTGAAATGGGGCTGTGAGGCGCGCTGTGCGAGTGCACAGACATTT 1767

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QY 1770 GACCTTAGTCTCCGGAACTGTGACCGCTGACAGCAGGTGTCTGAAGTGCATCCAC 1829
Db 1768 GATCCCAAGCTGTGTGGCAATGTGCAACCGGACAGCGGGGAGTGCCTCAAGTGCATCAC 1827
QY 1830 AACACAGCTGGGGTCCATCTGTACACAGTGCAAAGCAGGCTACTATGAGGGAACCGTTGGCT 1889
Db 1828 AACACAGCGGGCTTCTACTGTGCGACCGCTGCAAGACGGCTTCTTGGGAACCCCTGGCC 1887
QY 1890 CCCAATCCAGACAGCAAGTGTGAGCTTGCACCTGCACCTGACAGTGGGCTCGGAGCCTGTG 1949
Db 1888 ACCAACCTGTGACAGAGTGTGGGCTTGTCACTGTATTCCTACGGCACCGTGAATCAG 1947
QY 1950 GAG 1952
Db 1948 CAG 1950

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Search completed: July 11, 2003, 11:21:44  
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